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T73147 yc67e02.s1
R5267 yg82c02.s1
AA038583 mi85d11.r
AZ587290 1M0394A20
AA683660 vr03d08.r
AA933986 on95f08.s
AA702879 zi80h09.s
AA4184887 mu46h03.r
AA654356 nf09h06.s
AA4431961 zw77a05.s
AA4431961 zw77a05.s
AA442866 ni79903.s
AA542866 ni79903.s
AA557718 ni176f08.s
AA542867 ni16f08.s
AA5583175 nn37d08.s
AA558718 ni17909.s
AA625891 zu87a06.s
AA5276214 AST-TD13S
AZ6478297 zw00149K10
AZ64783 2W0028E02
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AA972774 op90910.s
AA857783 oce42e03.s
AL429245 clone BA0
AU102680 AU102680
AA565659 nk26h02.s
AB630207 ab99907.s
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Post-processing: Minimum Match
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AJ303694 Plasmodiu
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AA833683 aJ37c11.s
AI020738 ub01h04.r
AL463861 T. brucei
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AA394031 zt85e11.r
D43017 D43017 Rice
AU107342 AU107342
AA194224 zq04c04.r
D25852 HUMGS04228
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AJ303694
AJ303694.1 GI:11140201
GSS; genome survey sequence.
Plasmodium chabaudi
Plasmodium chabaudi
Eukaryota; Alveolata; Apicomplexa; Ha
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                                                                                                                                 Janssen,C.S.
Direct Submission
Submitted (06-NOV-2000) Divisi
University of Glasgow, Joseph
bases 122 to 170 (OL to QR).
                                                                                                                                                                                                            Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harr Bowman,S., Phillips,R.S. and Turner,C.M. Gene discovery in Plasmodium chabaudi by genome survey Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
                                                                                                                                                                                                                                                                                                                                                PCH303694 49 bp
Plasmodium chabaudi c
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Conservative
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/db_xref="taxon:5825"
/clone="PC9h11.plt"
11 c 10 g 19 t
                                                                                                            Location/Qualifiers
1..49
          58.4%;
81.0%;
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Score 14.6; DB 13;
Pred. No. 1.1e+04;
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R638583

RA2587290

RA683660

RA933986

RA702879

RA68543887

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RA684586

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Joseph Black Building, Glasgow G12 8QQ,
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03-APR-2001 PC9h11.p1t,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: 0 column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg., 20
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/db_xref="taxon:10090"
/clone="UUGC1M0542015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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Best Local Similarity

56.8%; 84.2%;

Score 14.2; DB 13; Pred. No. 1.6e+04;

Length 39;

Query Match

56.0%;

Score 14;

DB 13;

Length 27;

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High quality sequence stop: 27.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0296 row: G column: 14
Seq primer: CACACAGGAAACAGCTATGACC
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AZ477331
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Fax: 801 585 7177
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University of Utah
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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               adaptored vector DNA, and transformed into. chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

6 c 5 g 7 t
                                                                                               adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gii4732114)gbiaFr129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                     was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                               musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0296G14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
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Best Local Similarity Matches 17; Conserv

Conservative

77.3%;

Pred. No. 1.9e+04; 0; Mismatches 5;

Indels

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                                                              34 TCCAAGATAGAATCTTGGTACA
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||||||||||| ||| || |||
3 TCCAACTTGTAATAAGGACACA
                                                                                             2 tccaacttggaatcacggtaca 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA833683 53 bp mRNA
aj37c11.s1 Soares_testis_NHT Homo
similar to gb:M73628 KAPPA CASEIN
                                                                                                                               l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                       /clone="1392500"
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
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                                                                                                                                            56.0%;
77.3%;
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                                                                                                                          Score 14; DB 10; Pred. No. 2.1e+04;
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                                                                                                                                                          Length 53;
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1 ctccaacttggaatcacggtacaca 25

CGCCAACTGTGTACCACGGCACGCA

36

Query Match Best Local

Similarity

Conservative

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Mismatches

Score 13.8; DB 10 Pred. No. 2.5e+04;

DB 10;

Length 43;

0;

Gaps

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Matches

TA129A09Q/c

LOCUS

RESULT

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DEFINITION

TA129A09Q 53 bp DNA GSS T. brucei sheared genomic DNA clone 129a09, genomic survey sequence.

reverse sequence, 13-DEC-2000

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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDEHYDE REDUCTASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality Possible reversed clone: similarity on w. Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
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Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                    10
                                                                                                                                                                                                        T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
                                                                                                                    Bonaldo."
                                                                                                                                                          RNA provided by Dr. Minoru Ko, Wayne State Univ. Librar constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                            /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1365751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NbMMG"
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55.2%;
72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrellesanger.ac.uk and nhlesanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kD). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                            Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Of The Noble Parkway, Ardmore, OK 73402,
2510 Sam Noble Parkway, Ardmore, Tel: 580 221 7391 Fax: 580 221 7380
                                                                                                                                     Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                  Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolicae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             nF011900 52 bp n
NF016F05DT1F1044 Drought
5'; mRNA segment
                                                                                                    Contact: May GD
                                                                                                                          Unpublished (2000)
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barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                      BF631900.1 GI:11896058
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Details of T. brucei sequencing at the Sanger Centre are at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                       Medicago.
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18; Conservative
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/clone="129a09"
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Pred. No. 2.5e+04;
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                                       USA
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||||| || || || |||||
ACTTGCAAACAAGCTACACA 29
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore, Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyl,T., Waterston,R. and Wilson,R.
Washu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA394031 52 bp mRNA EST 16-MP zt85e11.rl Soares_testis_NHT Homo sapiens cDNA clone IV 5' similar to WP:D1022.1 CE02575 UBIQUITIN-CONJUGATING
                                                                                                                                                                                                                                                    High quality sequence stop: 1.
Location/Qualifiers
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16; Conserv
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/Sex- "WALE" DHIOB"
/lab_host="DHIOB"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories was prepared from with a Not I - oligo(dT) primer [5/
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:5925693"
/db_xref="taxon:9606"
/clone="IMAGE:729164"
                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days post watering
                                                                                                                                     /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          timepoints.
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/tissue_type="Plantlets"
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/clone="NF016F05DT"
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one IMAGE:729164
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17; Conserv
                                       AU107342 50 bp mRNA EST 05-APR-2001 AU107342 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ADKAD2874, mRNA sequence.
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan
Tel: 03-3812-2111(ex.7844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Function
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(bases 1 to 60)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     huchimiy@tansei.cc.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOUBLE-Stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " a 9 c 19 g 12 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uchimiya.
                                                                                                                                                                                                                                                                                                                                                     /clone="AD344"
/clone_lib="Rice callus cDNA
/tissue_type="callus"
20 c 15 g 11 t
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/db_xref="taxon:4530"
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              GI:13556863
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73.9%;
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Pred. No. 3.8e+04;
0; Mismatches 6;
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Pred. No. 3.9e+04;
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(H.Uchimiya) Oryza
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukidims.u.tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitomo-Nakagawa,K., Gene 200 (1-2), 149-156 (1997).
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1 (bases 1 to 50)
Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries unpublished (2001)
                                                                                             This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further; Insert Length: 819 Std Error: 0.00
                                                                                                                                                                                                                                                                                           Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                High quality sequence stop: 1.
                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                       Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                              White,Y., Wylie,T., WaterstowashU-NCI human EST Project
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1 (bases 1 to 54)
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       /organism="Homo sapiens"
/db_xref="GDB:5048944"
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15 c 11 g
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/db_xref="taxon:9606"
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Pred. No. 5.8e+04;
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                                    yc67e02.sl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGB:85754 3′ similar to gb:X54486_rnal PLASMA PROTEASE C1
                                                                                                                                                                                                                                                                                                                                                                                        random cDNA sequencing analysis
Unpublished (1994)
Contact: Okubo,K., Itoh,K., Yoshii,J., Yokou
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 41) Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K. Global analysis of gene expression in colon mucosa: a large sc
                                                                T73147
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cm2172"
/clone="tb="Human colon mucosa"
/note="Adult male, tissue_type = cc
a 8 c 3 g 15 t
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                        mRNA sequence
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                                                                                                                                                                               47 bp mRNA EST 18-MAY-1995 yg82C02.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:39999 3' similar to gb|Ll3710|HUMSCALUH Human scRNA molecule, transcribed from Alu (rRNA); gb:M62424 THROMBIN RECEPTOR PRECURSOR
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Location/Qualifiers
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1 (bases 1 to 47)
                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Insert Size: 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
                                                                              human
                                                                                                                                                            (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 46)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:85754"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:814529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GDB:50281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.4%;
75.0%;
              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.6; DB 11;
Pred. No. 8.7e+04;
n. Mismatches 5;
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JOURNAL
                      TITLE
                                                                                                                              AUTHORS
                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                      AA038583 55 bp mRNA EST 28-AUG-1996 m185d11.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE.473397 5' similar to SW:KTHY_HUMAN P23919 THYMIDYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Insert Size: 1970
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
                                                      Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                              EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1996)
                    Waterston,R.
The WashU-HHMI Mouse
                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                AA038583.1 GI:1513989
                                                                                                                                                                                                                                                                                                       AA038583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
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314 286 1810
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10 c 17 g 10 t 3 others
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/db_xref="GDB:412540"
/db_xref="taxon:9606"
/clone="IMAGE:39999"
                                                                                                                                                1 to 55)
                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
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71.4%;
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               EST Project
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Pred. No. 8.7e+04;
0; Mismatches 6;
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15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of MedicineP
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                                                        Conservative
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                                                                                                                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by
                                                                                                                                                                          Dr. Minoru Ko (Wayne State University)." 13 \text{ c} 23 \text{ g} 10 \text{ t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:473397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                        50.4%;
78.9%;
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Pred. No. 8.9e
0; Mismatches
                                                                           8.9e+04;
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